

SEQUENCE LISTING

<110> Asundi, Vinod
 Ford, John E.
 Drmanac, Radoje T
 Liu, Chenghua
 Tang, Y. Tom
 Yamasaki, Vicky
 Yeung, George
 Zhang, Jie
 Zhou, Ping
 Zhou, Hua

<120> EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS

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<150> US 09/687,860

<151> 2000-10-13

<150> US 09/620,312

<151> 2000-07-19

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gga tgt aag ttt ggt gag tgc gtg gga	cca aac aaa tgc aga tgc ttt	96
Gly Cys Lys Phe Gly Glu Cys Val Gly	Pro Asn Lys Cys Arg Cys Phe	
20	25 30	

cca gga tac acc ggg aaa acc tgc agt	caa gat gtg aat gag tgt gga	144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser	Gln Asp Val Asn Glu Cys Gly	
35	40 45	

atg aaa ccc cgg cca tgc caa cac aga	tgt gtg aat aca cac gga agc	192
Met Lys Pro Arg Pro Cys Gln His Arg	Cys Val Asn Thr His Gly Ser	
50	55 60	

tac aag tgc ttt tgc ctc agt ggc cac	atg ctc atg cca gat gct acg	240
Tyr Lys Cys Phe Cys Leu Ser Gly His	Met Leu Met Pro Asp Ala Thr	
65	70 75 80	

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
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Glu	Asp	Thr	Glu													
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1				5					10					15		

gga	tgt	aag	ttt	ggt	gag	tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	96
Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	
			20					25					30			

cca	gga	tac	acc	ggg	aaa	acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	144
Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	
		35					40					45				

atg	aaa	ccc	cgg	cca	tgc	caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	192
Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	
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tac	aag	tgc	ttt	tgc	ctc	agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	240
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	
65					70					75					80	

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
				85					90					95		

gaa	gac	aca	gaa	gaa	ggg	cca	cag	tgc	ctg	tgt	cca	tcc	tca	gga	ctc	336
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	
			100					105					110			

cgc	ctg	gcc	cca	aat	gga	aga	gac	tgt	cta	gat	att	gat	gaa	tgt	gcc	384
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	
		115					120					125				

tct	ggt	aaa	gtc	atc	tgt	ccc	tac	aat	cga	aga	tgt	gtg	aac	aca	ttt	432
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
	130					135					140					

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Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	
145					150					155					160	

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cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe 180 185 190	576
aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser 195 200 205	624
gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr 210 215 220	672
atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys 225 230 235 240	720
aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro 245 250 255	768
acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser 260 265 270	816
aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met 275 280 285	864
aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn 290 295 300	912
gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val 305 310 315 320	960
aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu 325 330 335	1008
act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser 340 345 350	1056
ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe 355 360 365	1104
gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala 370 375 380	1152
gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu 385 390 395 400	1200
ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp 405 410 415	1248

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1 5 10 15

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Pro 25	Gly 40	Tyr 55	Thr 70	Gly 85	Lys 100	Thr 115	Cys 130	His 145	Gln 160	Asp 175	Val 190	Asn 205	Glu 220	Cys 235	Gly 250
Met 60	Lys 75	Pro 90	Arg 105	Pro 120	Cys 135	Gln 150	His 165	Arg 180	Cys 195	Val 210	Asn 225	Thr 240	His 255	Gly 270	Ser 285
Tyr 65	Lys 80	Cys 95	Phe 110	Cys 125	Leu 140	Ser 155	Gly 170	His 185	Met 200	Leu 215	Met 230	Pro 245	Asp 260	Ala 275	Thr 290
Cys 70	Val 85	Asn 100	Ser 115	Arg 130	Thr 145	Arg 160	Cys 175	Ala 190	Met 205	Ile 220	Cys 235	Gln 250	Tyr 265	Ser 280	Cys 295
Glu 75	Asp 90	Thr 105	Glu 120	Gly 135	Pro 150	Gln 165	Cys 180	Leu 195	Cys 210	Pro 225	Ser 240	Ser 255	Gly 270	Gly 285	Leu 295
Arg 80	Leu 95	Ala 110	Pro 125	Asn 140	Gly 155	Arg 170	Asp 185	Cys 200	Leu 215	Asp 230	Ile 245	Asp 260	Glu 275	Cys 290	Ala 295
Ser 85	Gly 100	Lys 115	Val 130	Ile 145	Cys 160	Pro 175	Tyr 190	Asn 205	Arg 220	Arg 235	Cys 250	Val 265	Asn 280	Thr 295	Phe 300
Gly 90	Ser 105	Tyr 120	Tyr 135	Cys 150	Lys 165	Cys 180	His 195	Ile 210	Gly 225	Phe 240	Glu 255	Leu 270	Gln 285	Tyr 295	Ile 300
Ser 95	Gly 110	Arg 125	Tyr 140	Asp 155	Cys 170	Ile 185	Asp 200	Ile 215	Asn 230	Glu 245	Cys 260	Thr 275	Met 290	Asp 295	Ser 300
His 100	Thr 115	Cys 130	Ser 145	His 160	His 175	Ala 190	Asn 205	Cys 220	Phe 235	Asn 250	Thr 265	Gln 280	Gly 295	Ser 300	Phe 305
Lys 105	Cys 120	Lys 135	Cys 150	Lys 165	Gln 180	Gly 195	Tyr 210	Lys 225	Gly 240	Asn 255	Gly 270	Leu 285	Arg 295	Cys 300	Ser 305
Ala 110	Ile 125	Pro 140	Glu 155	Asn 170	Ser 185	Val 200	Lys 215	Glu 230	Val 245	Leu 260	Arg 275	Ala 290	Pro 295	Gly 300	Thr 305
Ile 115	Lys 130	Asp 145	Arg 160	Ile 175	Lys 190	Lys 205	Leu 220	Leu 235	Ala 250	His 265	Lys 280	Asn 295	Ser 300	Met 305	Lys 310
Lys 120	Lys 135	Ala 150	Lys 165	Ile 180	Lys 195	Asn 210	Val 225	Thr 240	Pro 255	Glu 270	Pro 285	Thr 295	Arg 300	Thr 305	Pro 310
Thr 125	Pro 140	Lys 155	Val 170	Asn 185	Leu 200	Gln 215	Pro 230	Phe 245	Asn 260	Tyr 275	Glu 290	Glu 295	Ile 300	Val 305	Ser 310
Arg 130	Gly 145	Gly 160	Asn 175	Ser 190	His 205	Gly 220	Gly 235	Lys 250	Lys 265	Gly 280	Asn 295	Glu 300	Glu 305	Lys 310	Met 315
Lys 135	Glu 150	Gly 165	Leu 180	Glu 195	Asp 210	Glu 225	Lys 240	Arg 255	Glu 270	Glu 285	Lys 300	Ala 305	Leu 310	Lys 315	Asn 320
Asp 305	Ile 320	Glu 335	Glu 350	Arg 365	Ser 380	Leu 395	Arg 410	Gly 425	Asp 440	Val 455	Phe 470	Phe 485	Pro 500	Lys 515	Val 530
Asn 310	Glu 325	Ala 340	Gly 355	Glu 370	Phe 385	Gly 400	Leu 415	Ile 430	Leu 445	Val 460	Gln 475	Arg 490	Lys 505	Ala 520	Leu 535
Thr 315	Ser 330	Lys 345	Leu 360	Glu 375	His 390	His 405	Lys 420	Leu 435	Asn 450	Ile 465	Arg 480	Ser 495	Val 510	Asp 525	Ser 540
Phe 320	Asn 335	His 350	Gly 365	Ile 380	Cys 395	Asp 410	Trp 425	Lys 440	Gln 455	Asp 470	Arg 485	Arg 500	Glu 515	Asp 530	Phe 545
Asp 325	Trp 340	Asn 355	Pro 370	Ala 385	Asp 400	Arg 415	Asp 430	Asn 445	Ala 460	Ile 475	Gly 490	Phe 505	Tyr 520	Met 535	Ala 550
Val 330	Pro 345	Ala 360	Leu 375	Ala 390	Gly 405	His 420	Met 435	Lys 450	Asp 465	Ile 480	Gly 495	Arg 510	Leu 525	Lys 540	Leu 555
Leu 335	Leu 350	Pro 365	Asp 380	Leu 395	Gln 410	Pro 425	Gln 440	Ser 455							

Tyr Val Ser Ser Leu Val Phe Leu Ile Leu His His Arg Thr Ser Gly
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Ile Leu Lys Leu Leu Ala Glu Lys Leu
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ggaggc	ggcg	gcttag	ctgc	tacggg	gtcc	ggcggc	gcc	ctccc	gaggg	gggtc	cagga		180			
ggagga	aagga	ggaccc	gtgc	gaga	atg	cct	ctg	ccc	tgg	agc	ctt	gcg	ctc	231		
				Met	Pro	Leu	Pro	Trp	Ser	Leu	Ala	Leu				
				1				5								
ccg	ctg	ctg	ctc	ccc	tgg	gtg	gca	ggg	ggg	ttc	ggg	aac	gcg	gcc	agt	279
Pro	Leu	Leu	Leu	Pro	Trp	Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	
10					15					20					25	
gca	agg	cat	cac	ggg	ttg	tta	gca	tcg	gca	cgt	cag	cct	ggg	gtc	tgt	327
Ala	Arg	His	His	Gly	Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	
				30					35					40		
cac	tat	gga	act	aaa	ctg	gcc	tgc	tgc	tac	ggc	tgg	aga	aga	aac	agc	375
His	Tyr	Gly	Thr	Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	
			45					50						55		
aag	gga	gtc	tgt	gaa	gct	aca	tgc	gaa	cct	gga	tgt	aag	ttt	ggg	gag	423
Lys	Gly	Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	
		60					65					70				
tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	cca	gga	tac	acc	ggg	aaa	471
Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	
	75					80					85					
acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	cca	tgc	519
Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
90					95					100					105	
caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	tac	aag	tgc	ttt	tgc	ctc	567
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	
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agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	tgt	gtg	aac	tct	agg	aca	615
Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	
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tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	gaa	gac	aca	gaa	gaa	ggg	663
Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	
		140					145					150				
cca	cag	tgc	ctg	tgt	cca	tcc	tca	gga	ctc	cgc	ctg	gcc	cca	aat	gga	711
Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	
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Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac wta gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Xaa Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	

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Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly
430 435 440

cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa 1575
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln
445 450 455

ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac 1623
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp
460 465 470

aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg 1671
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu
475 480 485

gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa 1719
Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys
490 495 500 505

att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa 1767
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu
510 515 520

gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc 1815
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val
525 530 535

ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac 1863
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
540 545 550

tga atgttactat ctttatatatt gactttgtat gtcagttccc tgggttttttt 1916
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35 40 45

00001519 101501

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Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn
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Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr
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His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro
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Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Glu
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Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser
145				150						155				160	
Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp
				165					170					175	
Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val
			180					185					190		
Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu
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Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr
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Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln
225				230						235				240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu
			245						250					255	
Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala
			260					265					270		
Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn
		275					280					285			
Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr
	290				295						300				
Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu
305				310						315					320
Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu
				325					330					335	
Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala
			340					345					350		
Leu	Lys	Asn	Asp	Xaa	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe
		355					360					365			
Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg
	370					375						380			
Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val
385				390						395				400	
Asp	Cys	Ser	Phe	Asn	His	Gly	Ile								

Pro Asp Ser Leu Leu Ser Val Asp Asp
545 550

<210> 7
<211> 42
<212> PRT
<213> Drosophila Melanogaster

<220>
<221> VARIANT
<222> (1)...(42)
<223> Xaa = Any Amino Acid

<400> 7
Ile Asp Glu Cys Xaa Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Xaa
1 5 10 15
Xaa Xaa Asp Xaa Val Gly Ser Tyr Xaa Cys Xaa Cys Pro Pro Gly Phe
20 25 30
Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn
35 40

<210> 8
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(39)
<223> Xaa = Any Amino Acid

<400> 8
Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys Gln His Xaa Xaa Xaa Cys
1 5 10 15
Val Asn Thr Xaa Gly Ser Tyr Xaa Cys Lys Cys Xaa Ser Gly Xaa Xaa
20 25 30
Gly Xaa Xaa Leu Xaa Cys Asp
35

<210> 9
<211> 164
<212> PRT
<213> Homo sapiens

<400> 9
Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Val Asn
1 5 10 15
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
20 25 30
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
35 40 45
Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
50 55 60
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
65 70 75 80
Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys
85 90 95
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys
100 105 110
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu
115 120 125
Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn
130 135 140

0998649-101501

Thr Gln Gly Ser Phe Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly
 145 150 155 160
 Leu Arg Cys Ser

<210> 10
 <211> 45
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(45)
 <223> Xaa = Any Amino Acid

<400> 10
 Val Xaa Glu Cys Xaa Ser Gly Xaa Gln Xaa Xaa Cys Xaa Ser Ser Xaa
 1 5 10 15
 Xaa Cys Xaa Asn Thr Val Gly Ser Tyr Xaa Cys Arg Cys Arg Pro Gly
 20 25 30
 Trp Xaa Pro Xaa Pro Gly Xaa Pro Asn Xaa Xaa Xaa Asp
 35 40 45

<210> 11
 <211> 58
 <212> PRT
 <213> Mammalian

<220>
 <221> VARIANT
 <222> (1)...(58)
 <223> Xaa = Any Amino Acid

<400> 11
 Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
 1 5 10 15
 Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 20 25 30
 Cys Val Val Gly Tyr Ile Xaa Xaa Xaa Gly Glu Arg Xaa Xaa Cys Gln
 35 40 45
 Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg
 50 55

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene-specific PCR primer 10244-52

<400> 12
 ctcacacctca agccctctt t

<210> 13
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene-specific PCR primer 10244-51

<400> 13

ccatgagagt tcccgcctct g 21

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector primer T7

<400> 14
gtaatacgac tcactatagg g 21

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector primer SP6

<400> 15
atttaggtga cactatagaa gg 22

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene-specific PCR primer 10244-A

<400> 16
cccaggtga cgtgccgatg c 21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene-specific PCR primer 10244-B

<400> 17
gcagcaggcc agtttagttc c 21

<210> 18
<211> 502
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(502)
<223> Xaa = Any Amino Acid

<400> 18
Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
1 5 10 15
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
20 25 30
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
35 40 45

Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser
50						55					60				
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr
65					70					75					80
Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys
				85					90					95	
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu
			100					105					110		
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala
		115					120					125			
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe
	130					135					140				
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile
145					150					155					160
Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser
				165					170					175	
His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe
			180					185					190		
Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser
		195					200					205			
Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr
	210					215					220				
Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys
225					230					235					240
Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro
			245						250					255	
Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser
			260					265					270		
Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met
		275					280					285			
Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn
	290					295					300				
Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val
305					310					315					320
Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu
			325						330					335	
Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser
			340					345					350		
Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe
		355					360					365			
Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala
	370					375					380				
Val	Pro	Ala	Leu	Ala	Gly	His	Met	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu
385					390					395					400
Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp
			405						410					415	
Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys
			420					425					430		
Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu
		435					440					445			
Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr
	450					455					460				
Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu
465					470					475					480
Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys	Pro	Asp	Ser
			485						490					495	
Leu	Leu	Ser	Val	Xaa	Xaa										
			500												

<210> 19

<211> 21

<212> DNA

<213> Artificial Sequence

00004649 104504

<220>

<223> Description of Artificial Sequence: primer

<400> 19

gtcattttctg aatctttcca c

21

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20

gaaatgttgc agagagaagc tc

22

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 21

ccagaaccca ccaggactcc

20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

gggaactgac atacaaagtc

<210> 23

<211> 2365

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (205)..(1863)

<400> 23

actagtgtatt ccatactaata acgactcact atagggctcg agcggccgcc cgggcaggtc 60

tgcagggaca gcacccggta actgcgagtg gagcggagga cccgagcggc tgaggagaga 120

ggagggggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccgaggg gggctcagga 180

ggaggaagga ggacccgtgc gaga atg cct ctg ccc tgg agc ctt gcg ctc 231

Met Pro Leu Pro Trp Ser Leu Ala Leu

1

5

ccg ctg ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt 279

Pro Leu Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser

10

15

20

25

gca agg cat cac ggg ttg tta gca tgg gca cgt cag cct ggg gtc tgt	327
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys	
30 35 40	
cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc	375
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser	
45 50 55	
aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag	423
Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu	
60 65 70	
tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa	471
Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys	
75 80 85	
acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc	519
Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys	
90 95 100 105	
caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc	567
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu	
110 115 120	
agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca	615
Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr	
125 130 135	
tgt gcc atg ata aac tgt cag tat agc tgt gaa gac aca gaa gaa ggg	663
Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly	
140 145 150	
cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga	711
Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly	
155 160 165	
aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	

00001649 101501

aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt	1527
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly	
430 435 440	
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa	1575
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln	
445 450 455	
ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac	1623
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp	
460 465 470	
aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg	1671
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu	
475 480 485	
gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa	1719
Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys	
490 495 500 505	
att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa	1767
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu	
510 515 520	
gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc	1815
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val	
525 530 535	

00001649-101504

ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac 1863
 Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
 540 545 550

tgaatgttac tatctttata tttagactttg tatgtcagtt ccctggtttt tttagatattg 1923
 satcatagga cctctggcat tttaaaatta ctaagctgaa aaattgtaat gtaccaacag 1983
 aaattattat tgtaagatgc ctttmttgta taagatatgc caatatttgc tttaaatatc 2043
 atatcactgt atcttctcag tcattttotga atctttccac attatattat aaaatatgga 2103
 aatgtcaggt ttatctcccc tcctcagtat atctgatttg tataagtaag ttgatgagct 2163
 tctctctgca acattttctag aaaatagaha aaaaagcaca gagaaatgtt taactgtttg 2223
 actcttatga tagtttttgg aaactatgac atcaaagata gacttttgcc taagtggctt 2283
 agctgggtct ttcataagcca aacttgata tttaaattct ttgtaataat aatatccaaa 2343
 tcataaaaaa aaaaaaaaaa aa 2365

<210> 24
 <211> 553
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(553)

<400> 24

Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu Ser Trp Val
 1 5 10 15
 Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His Gly Leu Leu
 20 25 30
 Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala
 35 40 45
 Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr
 50 55 60
 Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys
 65 70 75 80
 Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn
 85 90 95
 Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
 100 105 110
 His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
 115 120 125
 Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln
 130 135 140
 Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser
 145 150 155 160

Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser
485 490 495

Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr
500 505 510
Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys
515 520 525
Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys
530 535 540
Pro Asp Ser Leu Leu Ser Val Asp Asp
545 550

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
ccctggcatg ggagaagacc ac 22

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gtgatatgat atttaaagca aatattggca 30

<210> 27
<211> 2360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (190)..(1869)

<220>
<221> misc_feature
<222> (1)...(2360)
<223> n = a,t,c or g

<400> 27
cctctatatg catgctcgag cgcggncgca gtgtgatgga tatctgcaga attcggtta 60

ctcactatag ggctcgagcg gccgcccggg caggtgagga gagaggaggc ggcggcttag 120

ctgctacggg gtccgggccg gcgccctccc gaggggggct caggaggagg aaggaggacc 180

cgtgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc 228
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
1 5 10

tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg ggt tct	276
Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg Gly Ser	
14 19 24 29	
cat cat cat cat cat cac ggg ttg tta gca tgc gca cgt cag cct ggg	324
His His His His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly	
30 35 40 45	
gtc tgt cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga	372
Val Cys His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg	
46 51 56 61	
aac agc aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt	420
Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe	
62 67 72 77	
ggg gag tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc	468
Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr	
78 83 88 93	
ggg aaa acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg	516
Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg	
94 99 104 109	
cca tgc caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt	564
Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe	
110 115 120 125	
tgc ctc agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct	612
Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser	
126 131 136 141	
agg aca tgt gcc atg ata aac tgt cag tac agc tgt gaa gac aca gaa	660
Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu	
142 147 152 157	
gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca	708
Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro	
158 163 168 173	
aat gga aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc	756
Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val	
174 179 184 189	
atc tgt ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac	804
Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr	
190 195 200 205	
tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat	852
Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr	
206 211 216 221	
gac tgt ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc	900
Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser	
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cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc	948
His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys	
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Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu	
254 259 264 269	
aat tct gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga	1044
Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg	
270 275 280 285	
atc aag aag ttg ctt gct cac aaa aac agt atg aaa aag aag gca aaa	1092
Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys	
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att aaa aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg	1140
Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val	
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Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn	
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tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt	1236
Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu	
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gag gat gag aaa aga gaa gag aaa gcc ctg aag aat gac ata gag gag	1284
Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu	
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Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly	
366 371 376 381	
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Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu	
382 387 392 397	
gaa cat aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg	1428
Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly	
398 403 408 413	
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Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro	
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gct gat cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg	1524
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Ala Gly His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp	
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Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala	
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Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn	
478 483 488 493	
gcc ctg gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca	1716
Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr	
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 ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat 1812
 Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp
 526 531 536 541

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 Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val
 542 547 552 557

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 Asp Asp *
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 taaatatcat atcactgtat cttctcagtc atttctgaat ctttccacat tatattataa 2096
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 35 40 45
 Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys
 50 55 60
 Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys
 65 70 75 80
 Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr
 85 90 95
 Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln
 100 105 110
 His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser
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Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	
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Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	
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Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	
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Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	
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Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	
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Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asr	
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Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	
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Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	
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Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	Leu	
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Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	
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Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	
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Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	
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Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	
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Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	
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Lys	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	
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Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys
465 470 475 480

Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala
485 490 495

Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile
500 505 510

Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala
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cgtgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc 228
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
1 5 10
tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg cat cat 276
Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His
14 19 24 29
cac ggg ttg tta gca tgc gca cgt cag cct ggg gtc tgt cac tat gga 324
His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly
30 35 40 45
act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc aag gga gtc 372
Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val
46 51 56 61
tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag tgc gtg gga 420
Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly
62 67 72 77

0904141050

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Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser	
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caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac aga	516
Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg	
94 99 104 109	
tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc cac	564
Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His	
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Met Leu Met Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met	
126 131 136 141	
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Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys	
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Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys	
158 163 168 173	
cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt ccc tac aat	756
Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn	
174 179 184 189	
cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa tgt cac att	804
Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile	
190 195 200 205	
ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt ata gat ata	852
Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile	
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Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys	
222 227 232 237	
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Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys	
238 243 248 253	
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Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu	
254 259 264 269	
gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag aag ttg ctt	1044
Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu	
270 275 280 285	
gct cac aaa aac agt atg aaa aag aag gca aaa att aaa aat gtt acc	1092
Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr	
286 291 296 301	
cca gaa ccc acc agg act cct acc cct aag gtg aac ttg cag ccc ttc	1140
Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe	
302 307 312 317	
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Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys	
318 323 328 333	

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542 547 552	
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 35 40 45
 Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala
 50 55 60
 Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys
 65 70 75 80
 Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val
 85 90 95
 Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn
 100 105 110
 Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met
 115 120 125
 Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys
 130 135 140
 Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro
 145 150 155 160
 Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile
 165 170 175
 Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys
 180 185 190
 Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu
 195 200 205
 Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys
 210 215 220

05981649 101501

Thr 225	Met	Asp	Ser	His	Thr 230	Cys	Ser	His	Ala	Asn	Cys	Phe	Asn	Thr 240	
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Leu	Arg	Cys	Ser 260	Ala	Ile	Pro	Glu	Asn 265	Ser	Val	Lys	Glu	Val	Leu	Arg
Ala	Pro	Gly 275	Thr	Ile	Lys	Asp	Arg 280	Ile	Lys	Lys	Leu	Leu 285	Ala	His	Lys
Asn	Ser 290	Met	Lys	Lys	Lys	Ala 295	Lys	Ile	Lys	Asn	Val 300	Thr	Pro	Glu	Pro
Thr 305	Arg	Thr	Pro	Thr	Pro 310	Lys	Val	Asn	Leu	Gln 315	Pro	Phe	Asn	Tyr	Glu 320
Glu	Ile	Val	Ser	Arg 325	Gly	Gly	Asn	Ser	His 330	Gly	Gly	Lys	Lys	Gly	Asn 335
Glu	Glu	Lys 340	Met	Lys	Glu	Gly	Leu 345	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys
Ala	Leu	Lys 355	Asn	Asp	Ile	Glu	Glu 360	Arg	Ser	Leu	Arg	Gly 365	Asp	Val	Phe
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Arg 385	Lys	Ala	Leu	Thr	Ser 390	Lys	Leu	Glu	His	Lys 395	Asp	Leu	Asn	Ile	Ser 400
Val	Asp	Cys	Ser	Phe 405	Asn	His	Gly	Ile	Cys 410	Asp	Trp	Lys	Gln	Asp 415	Arg
Glu	Asp	Asp	Phe 420	Asp	Trp	Asn	Pro	Ala 425	Asp	Arg	Asp	Asn	Ala 430	Ile	Gly
Phe	Tyr 435	Met	Ala	Val	Pro	Ala	Leu 440	Ala	Gly	His	Lys	Lys 445	Asp	Ile	Gly
Arg 450	Leu	Lys	Leu	Leu	Leu	Pro 455	Asp	Leu	Gln	Pro	Gln 460	Ser	Asn	Phe	Cys
Leu 465	Leu	Phe	Asp	Tyr	Arg 470	Leu	Ala	Gly	Asp	Lys 475	Val	Gly	Lys	Leu	Arg 480
Val	Phe	Val	Lys 485	Asn	Ser	Asn	Asn	Ala	Leu 490	Ala	Trp	Glu	Lys	Thr 495	Thr
Ser	Glu	Asp	Glu 500	Lys	Trp	Lys	Thr	Gly 505	Lys	Ile	Gln	Leu	Tyr 510	Gln	Gly
Thr	Asp 515	Ala	Thr	Lys	Ser	Ile	Ile 520	Phe	Glu	Ala	Glu	Arg 525	Gly	Lys	Gly
Lys 530	Thr	Gly	Glu	Ile	Ala	Val 535	Asp	Gly	Val	Leu	Leu 540	Val	Ser	Gly	Leu
Cys 545	Pro	Asp	Ser	Leu	Leu 550	Ser	Val	Asp	Asp						

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Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu
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Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg
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His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr
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Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly
45 50 55
gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag tgc gtg 482
Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val
60 65 70 75
gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa acc tgc 530
Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys
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agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac 578
Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His
95 100 105
aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc 626
Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly
110 115 120
cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca tgt gcc 674
His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala
125 130 135
atg ata aac tgt cag tac agc tgt gaa gac aca gaa gaa ggg cca cag 722
Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln
140 145 150 155
tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga aga gac 770
Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp
160 165 170

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Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr	
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Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His	
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Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp	
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ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat gcc aat	962
Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn	
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tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag gga tat	1010
Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr	
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Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys	
255 260 265	
gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag aag ttg	1106
Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu	
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ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa aat gtt	1154
Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val	
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Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Val Asn Leu Gln Pro	
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly	
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Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys	
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Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg	
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Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu	
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Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala	
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0001649 401300

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415 420 425

gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac 1586
Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His
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aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc 1634
Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro
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Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys
460 465 470 475

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Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala
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Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
540 545 550 555

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<400> 32

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09961649-101E04

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Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala
35 40 45

Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr
50 55 60

Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys
65 70 75 80

Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn
85 90 95

Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
100 105 110

His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
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Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln
130 135 140

Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser
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Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp
165 170 175

Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val
180 185 190

Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu
195 200 205

Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr
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Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln
225 230 235 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu
245 250 255

Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala
260 265 270

Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn
275 280 285

Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr
290 295 300

Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu
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Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu
325 330 335

Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala
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09901649 101504

Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe
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 Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg
 370 375 380
 Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala Asp Leu Asn Ile Ser
 385 390 395 400
 Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg
 405 410 415
 Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly
 420 425 430
 Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly
 435 440 445
 Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys
 450 455 460
 Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg
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 485 490 495
 Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly
 500 505 510
 Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly
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 Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu
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 Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
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